

10/581757

SEQUENCE ~~1AP20 Rec'd PCT/PTO 05 JUN 2006~~

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ASAKURA, MASAHIRO

<120> CYTOLETHAL DISTENDING TOXINS AND DETECTION OF
CAMPYLOBACTER BACTERIA USING THE SAME AS A TARGET

<130> SHIM-018

<150> JP 2003-408103
<151> 2003-12-05

<160> 79

<170> PatentIn version 3.1

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Phe Leu Ala Cys Ser Ser Lys Glu Gln Gln Ile Asn Pro Leu Gly Arg
20 25 30

tct tac ggt aaa ttt aac gat aac gat cct tta aaa ctt ggt tca aaa 144
Ser Tyr Gly Lys Phe Asn Asp Asn Asp Pro Leu Lys Leu Gly Ser Lys
35 40 45

cct aca ccc cct gtc aaa caa aaa aca cca agc ttg gta gaa ggt aaa 192
Pro Thr Pro Pro Val Lys Gln Lys Thr Pro Ser Leu Val Glu Gly Lys
50 55 60

aaa ttt ccc gcc ata cca ctt gtc cca cct gta atc act cct aat acc 240
Lys Phe Pro Ala Ile Pro Leu Val Pro Pro Val Ile Thr Pro Asn Thr
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ttt aaa gga gat aat gcc gtc aaa ggc cca ttg cca agg cta aaa tct 288
Phe Lys Gly Asp Asn Ala Val Lys Gly Pro Leu Pro Arg Leu Lys Ser
85 90 95

cca aac gaa ttt gct tca aat gct tta tac gaa aac aca ggt atg gta Pro Asn Glu Phe Ala Ser Asn Ala Leu Tyr Glu Asn Thr Gly Met Val 100 105 110	336
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aac aat aca gta atg att aaa aat gca aaa aca ttt act tgc tta aac Asn Asn Thr Val Met Ile Lys Asn Ala Lys Thr Phe Thr Cys Leu Asn 165 170 175	528
gcc tat aga aat ggc atc gtt cat tat cct tgt gat caa aca aat ttt Ala Tyr Arg Asn Gly Ile Val His Tyr Pro Cys Asp Gln Thr Asn Phe 180 185 190	576
gcf cag ttt tgg aga ctt tat ccg atg act aat gga gct tat caa att Ala Gln Phe Trp Arg Leu Tyr Pro Met Thr Asn Gly Ala Tyr Gln Ile 195 200 205	624
caa aat ttt gcc acc caa caa tgt ata caa aca cct gtt tca aat gta Gln Asn Phe Ala Thr Gln Gln Cys Ile Gln Thr Pro Val Ser Asn Val 210 215 220	672
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Thr Pro Arg Gln Val Gln Pro Val Gly Val Gly Ile Pro Ile His Glu			
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Tyr Ile Trp Asn Leu Gly Ser Val Ser Arg Pro Ser Ser Val Tyr Ile			
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Tyr Tyr Ser Arg Val Asp Val Gly Ala Asn Arg Val Asn Leu Ala Ile			
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Val Ser Arg Val Gln Ala Asp Glu Val Phe Val Leu Pro Pro Thr			
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Val Ala Ser Arg Pro Ile Ile Gly Ile Arg Ile Gly Asn Asp Ala Phe			
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Phe Asn Ile His Ala Leu Ala Ser Gly Gly Asn Asp Ala Gly Ala Ile			
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Met Ile Leu Gly Asp Phe Asn Arg Glu Ser Gly Ala Leu Val Thr Leu			
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Leu Asp Pro Asp Leu Arg Ala Arg Thr Arg Val Val Val Pro Pro Ser			
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Ser Thr Gln Thr Ser Gly Arg Thr Ile Asp Tyr Ala Ile Thr Gly Asn			
475	480	485	
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Ser Asn Thr Ala Ala Leu Tyr Asn Pro Pro Ile Val Ala Ile Leu			
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Ala Leu Glu Gly Leu Arg Thr Phe Leu Ala Ser Asp His Phe Pro Val			
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Asn Phe Arg Arg Pro			
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Phe Ala Leu Leu Ser Phe Leu Lys Ala Glu Pro Ser Leu Asp Glu Leu			
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gca gac ttt act cct atg ttt gct ata aga tct tta gaa aca gga att			1734

Ala Asp Phe Thr Pro Met Phe Ala Ile Arg Ser Leu Glu Thr Gly Ile				
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tct tta agt cct ttt aga aaa act tca aaa agg tta gaa gat caa aat				1782
Ser Leu Ser Pro Phe Arg Lys Thr Ser Lys Arg Leu Glu Asp Gln Asn				
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Trp Phe Leu Lys Glu Ile Val Ala Asn Asp Glu Leu Lys Ala Arg Asp				
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Met His Ala Lys Asp Leu Pro Phe Gly Tyr Val Gln Phe Ile Ser Pro				
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agg ggc gat gat ata tgc cta gct gtt tta agt gaa aaa agt ttt ggc				1926
Arg Gly Asp Asp Ile Cys Leu Ala Val Leu Ser Glu Lys Ser Phe Gly				
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acc aaa tct tgc aaa caa gat ttg caa gat gga aca atg cag act att				1974
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Phe Ser Ile Ile Pro Met Thr Asn Gly Ser Ile Gln Ile Arg Ser Leu				
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acc aat ggt ggc aat caa tgc atg agc act ttt cct gac tct agt atc				2070
Thr Asn Gly Gly Asn Gln Cys Met Ser Thr Phe Pro Asp Ser Ser Ile				
665	670	675		
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Ala Ile Glu Asn Arg Phe Gly Leu Gly Glu Cys Leu Leu Asp Arg Ser				
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Ile Val Thr Val Leu Ser Lys Leu Phe Phe Phe Ser Pro Ala Ile Ile				
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Ser Tyr Gly Lys Phe Asn Asp Asn Asp Pro Leu Lys Leu Gly Ser Lys				
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 Phe Lys Gly Asp Asn Ala Val Lys Gly Pro Leu Pro Arg Leu Lys Ser
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 Pro Asn Glu Phe Ala Ser Asn Ala Leu Tyr Glu Asn Thr Gly Met Val
 100 105 110
 Ser Asp Phe Val Thr Ile Met Asn Pro Asn Gly Ala Ser Leu Thr Ile
 115 120 125
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 Ser Arg Pro Phe Gly Asp Ala Arg Ala Trp Gln Leu Ile Glu Phe Pro
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 Ala Tyr Arg Asn Gly Ile Val His Tyr Pro Cys Asp Gln Thr Asn Phe
 180 185 190
 Ala Gln Phe Trp Arg Leu Tyr Pro Met Thr Asn Gly Ala Tyr Gln Ile
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 Gln Asn Phe Ala Thr Gln Gln Cys Ile Gln Thr Pro Val Ser Asn Val
 210 215 220
 Met Glu Glu Phe Asn Leu Ser Phe Tyr Asn Ile Tyr Leu Thr Asp Cys
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 Ala Ala Thr Glu Ser Lys Trp Asn Val Ser Ile Arg Gln Leu Ile Thr
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 Gly Ala Asn Pro Met Asp Val Leu Ala Val Gln Glu Ala Gly Val Leu

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Pro Ser Ser Val Tyr Ile Tyr Tyr Ser Arg Val Asp Val Gly Ala Asn			
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Arg Val Asn Leu Ala Ile Val Ser Arg Val Gln Ala Asp Glu Val Phe			
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Val Leu Pro Pro Pro Thr Val Ala Ser Arg Pro Ile Ile Gly Ile Arg			
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Ile Gly Asn Asp Ala Phe Phe Asn Ile His Ala Leu Ala Ser Gly Gly			
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Asn Asp Ala Gly Ala Ile Val Ala Ala Val Asp Met Phe Phe Arg Asn			
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Arg Pro Asp Ile Asn Trp Met Ile Leu Gly Asp Phe Asn Arg Glu Ser			
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Gly Ala Leu Val Thr Leu Leu Asp Pro Asp Leu Arg Ala Arg Thr Arg			
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Gly	Tyr	Val	Gln	Phe	Ile	Ser	Pro	Arg	Gly	Asp	Asp	Ile	Cys	Leu	Ala
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Gly	Glu	Cys	Leu	Leu	Asp	Arg	Ser	Ile	Val	Thr	Val	Leu	Ser	Lys	Leu
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<223> an artificially synthesized primer sequence

<400> 48
ctaatcgtgt aaattttagct atagtt

26

<210> 49
<211> 23
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 49
tttttcaata tccatgcttt agc

23

<210> 50
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <223> an artificially synthesized primer sequence

 <400> 50
 tggatgatag caggggattt taa

23

<210> 51
 <211> 2180
 <212> DNA
 <213> Campylobacter fetus

<220>
 <221> CDS
 <222> (1)..(702)

<220>
 <221> CDS
 <222> (778)..(1629)

<220>
 <221> CDS
 <222> (1632)..(2177)

<400> 51
 atg act aaa att att ttc aag cat att aaa aat agt ctt att tta cta
 Met Thr Lys Ile Ile Phe Lys His Ile Lys Asn Ser Leu Ile Leu Leu
 1 5 10 15

48

ttt tgt atc gct ctt ttt agt gct tgc tca tca aaa acg aca aat gta
 Phe Cys Ile Ala Leu Phe Ser Ala Cys Ser Ser Lys Thr Thr Asn Val
 20 25 30

96

agc act caa aaa ata aat cca tta gga agc att ttt ggc aaa acg gat
 Ser Thr Gln Lys Ile Asn Pro Leu Gly Ser Ile Phe Gly Lys Thr Asp
 35 40 45

144

gat cca gat cca cta aat tta ggc gat ttt cca act ctt cta aca tca
 Asp Pro Asp Pro Leu Asn Leu Gly Asp Phe Pro Thr Leu Leu Thr Ser
 50 55 60

192

aat ttt aca aat cct atg ccg act aga acg cca tcg cca ctt aaa aaa
 Asn Phe Thr Asn Pro Met Pro Thr Arg Thr Pro Ser Pro Leu Lys Lys
 65 70 75 80

240

gtg gat ttg cct gta atg aac tca tta aca cat ggt ccg atg ttt tca
 Val Asp Leu Pro Val Met Asn Ser Leu Thr His Gly Pro Met Phe Ser
 85 90 95

288

agt gct ttt agt aaa ccg gac ttg aat ttc aaa caa cct act atc agt Ser Ala Phe Ser Lys Pro Asp Leu Asn Phe Lys Gln Pro Thr Ile Ser 100 105 110	336
cta caa ggt atc ccg cct gat cta ttt gat aga aca agc gat ttt atg Leu Gln Gly Ile Pro Pro Asp Leu Phe Asp Arg Thr Ser Asp Phe Met 115 120 125	384
gtg ata atg ggt gca aac ggc gtt gtg atc act att tgg tac aca tct Val Ile Met Gly Ala Asn Gly Val Val Ile Thr Ile Trp Tyr Thr Ser 130 135 140	432
cct gga aac tgg tta tgg ggc tac tcg ctc tat gaa agc ggc aat tta Pro Gly Asn Trp Leu Trp Gly Tyr Ser Leu Tyr Glu Ser Gly Asn Leu 145 150 155 160	480
gga gga tat cgt gtt tgg cgt cta att tta cta cca aat aat gaa gtc Gly Gly Tyr Arg Val Trp Arg Leu Ile Leu Leu Pro Asn Asn Glu Val 165 170 175	528
atg ata gta aat ttc aac act cgc acg act tgc ata aat act tat aaa Met Ile Val Asn Phe Asn Thr Arg Thr Thr Cys Ile Asn Thr Tyr Lys 180 185 190	576
aac gga gta att cac tca cct tgc aat aaa gat aat cct ttt cag aaa Asn Gly Val Ile His Ser Pro Cys Asn Lys Asp Asn Pro Phe Gln Lys 195 200 205	624
ttt acg ttt cgt cca atg aca aac gga gcc gta caa att tat aac aaa Phe Thr Phe Arg Pro Met Thr Asn Gly Ala Val Gln Ile Tyr Asn Lys 210 215 220	672
gct act aat tgc gtg ctt gca aac gcc tgt taataatcta ttcggttttg Ala Thr Asn Cys Val Leu Ala Asn Ala Cys 225 230	722
acgtttttgg ggcgataaat cttacgacaa aatgcactga tactatcgat caaca atg Met 235	780
gta ttt gct ccc gcc gca agt tgg aag act att tta tta gga gta Val Phe Ala Pro Ala Ala Ser Trp Lys Thr Ile Leu Leu Gly Val 240 245 250	828
aaa atg cga aat gtt att atg att ata ttt ata gca act tta ggc ttt Lys Met Arg Asn Val Ile Met Ile Ile Phe Ile Ala Thr Leu Gly Phe 255 260 265	876
gca aaa cca gaa gat tat aaa att gct act tgg aat ttg caa ggc agt Ala Lys Pro Glu Asp Tyr Lys Ile Ala Thr Trp Asn Leu Gln Gly Ser 270 275 280	924
tcg gct ata acc gaa agc aaa tgg aat ata agc gta cgt caa ata att Ser Ala Ile Thr Glu Ser Lys Trp Asn Ile Ser Val Arg Gln Ile Ile 285 290 295	972
agc ggt gaa aat cca gca gat ata tta gcc gtt caa gaa gca gga aat Ser Gly Glu Asn Pro Ala Asp Ile Leu Ala Val Gln Glu Ala Gly Asn	1020

300	305	310	315	
tta cct caa acc gct ctt cct aca ggt aga agc ata aat caa ggc ggc Leu Pro Gln Thr Ala Leu Pro Thr Gly Arg Ser Ile Asn Gln Gly Gly 320		325		330
acg atc gta act gag cat tta tgg cag cta ggc agt ata tct aga ccg Thr Ile Val Thr Glu His Leu Trp Gln Leu Gly Ser Ile Ser Arg Pro 335	340		345	1116
ttc caa gtc tat ata tat tat gct caa atc gac aca ggg gca aat aga Phe Gln Val Tyr Ile Tyr Tyr Ala Gln Ile Asp Thr Gly Ala Asn Arg 350	355		360	1164
gta aat tta gca atc gtt tca cgc ata aaa gct gat gaa atc atc atc Val Asn Leu Ala Ile Val Ser Arg Ile Lys Ala Asp Glu Ile Ile Ile 365	370		375	1212
ttg ccg cct acg gta gct tct cgt ccg ctc ata ggt ata aga ata Leu Pro Pro Pro Thr Val Ala Ser Arg Pro Leu Ile Gly Ile Arg Ile 380	385	390		1260
gga aac gac gta ttt ttc aac ata cac gct cta gca aat ggc gga gtc Gly Asn Asp Val Phe Phe Asn Ile His Ala Leu Ala Asn Gly Gly Val 400	405		410	1308
gat gct ccg gcg ata ata aat tca ata ttt gac aga ttt aga aat atg Asp Ala Pro Ala Ile Ile Asn Ser Ile Phe Asp Arg Phe Arg Asn Met 415	420		425	1356
cca aat atc act tgg atg att tta ggc gat ttt aac cgc tca cct gag Pro Asn Ile Thr Trp Met Ile Leu Gly Asp Phe Asn Arg Ser Pro Glu 430	435		440	1404
agt tta aga gga act ctt gga tta gaa act cgc gtc aga gta acg ttt Ser Leu Arg Gly Thr Leu Gly Leu Glu Thr Arg Val Arg Val Thr Phe 445	450		455	1452
tta aca cct ccg gcg cct act caa aga agc ggc gga acg ctt gac tgg Leu Thr Pro Pro Ala Pro Thr Gln Arg Ser Gly Gly Thr Leu Asp Trp 460	465	470		1500
gct ata gtt gga aac tca gcc ggc gat ctt gtc cga act acg ctt gta Ala Ile Val Gly Asn Ser Ala Gly Asp Leu Val Arg Thr Thr Leu Val 480	485		490	1548
gca gta ttg atg cta gca aac ctg cgg act cac cta gtt tcg gac cat Ala Val Leu Met Leu Ala Asn Leu Arg Thr His Leu Val Ser Asp His 495	500		505	1596
ttt ccg gta aat ttt aga aaa ttt gga gat aac ta atg aaa gct tta Phe Pro Val Asn Phe Arg Lys Phe Gly Asp Asn Met Lys Ala Leu 510	515		520	1643
gca ata ata ttt tta ttt gta agc ata agt ttt gca aac gaa aac ata Ala Ile Ile Phe Leu Phe Val Ser Ile Ser Phe Ala Asn Glu Asn Ile 525	530		535	1691
acc gac gct ttt caa ata cgc aat gca aac acc gga att cct ata aat 20				1739

Thr Asp Ala Phe Gln Ile Arg Asn Ala Asn Thr Gly Ile Pro Ile Asn			
540	545	550	
ata aag cga ttt tca ggg cag ttt aat tac caa aac tgg ttt tta aat			1787
Ile Lys Arg Phe Ser Gly Gln Phe Asn Tyr Gln Asn Trp Phe Leu Asn			
555	560	565	570
gat tta gga gta gat cct aag ata aaa aaa gta gat aaa ttt tca aat			1835
Asp Leu Gly Val Asp Pro Lys Ile Lys Lys Val Asp Lys Phe Ser Asn			
575	580	585	
tct ttt cct ttt gga tac gtg caa ttt caa gta gca gcc gac gta aaa			1883
Ser Phe Pro Phe Gly Tyr Val Gln Phe Gln Val Ala Ala Asp Val Lys			
590	595	600	
atg tgc ctt cag atc gct cct agc gga ttt tta gca cta aaa aac tgc			1931
Met Cys Leu Gln Ile Ala Pro Ser Gly Phe Leu Ala Leu Lys Asn Cys			
605	610	615	
aag caa gac tac gat agc gga gag ttt gag act att ttt cag atc atc			1979
Lys Gln Asp Tyr Asp Ser Gly Glu Phe Glu Thr Ile Phe Gln Ile Ile			
620	625	630	
cct aca agt agt gga gct atg cag cta cga tca cta gtt cta aaa aca			2027
Pro Thr Ser Ser Gly Ala Met Gln Leu Arg Ser Leu Val Leu Lys Thr			
635	640	645	650
aac gag tgc tta gga aca ttt gaa aat cca aac gtg ccg atc gaa gat			2075
Asn Glu Cys Leu Gly Thr Phe Glu Asn Pro Asn Val Pro Ile Glu Asp			
655	660	665	
aga gta gga cta gta cgc tgc gtt tta gaa ttt ttt gtc gac ata gag			2123
Arg Val Gly Leu Val Arg Cys Val Leu Glu Phe Phe Val Asp Ile Glu			
670	675	680	
cct aaa caa ctt ttt gta ttt tca ccg ccg ctt agt gaa gct aag gta			2171
Pro Lys Gln Leu Phe Val Phe Ser Pro Pro Leu Ser Glu Ala Lys Val			
685	690	695	
att aga taa			2180
Ile Arg			
700			
<210> 52			
<211> 234			
<212> PRT			
<213> Campylobacter fetus			
<400> 52			
Met Thr Lys Ile Ile Phe Lys His Ile Lys Asn Ser Leu Ile Leu Leu			
1	5	10	15
Phe Cys Ile Ala Leu Phe Ser Ala Cys Ser Ser Lys Thr Thr Asn Val			
20	25	30	

Ser Thr Gln Lys Ile Asn Pro Leu Gly Ser Ile Phe Gly Lys Thr Asp
35 40 45

Asp Pro Asp Pro Leu Asn Leu Gly Asp Phe Pro Thr Leu Leu Thr Ser
50 55 60

Asn Phe Thr Asn Pro Met Pro Thr Arg Thr Pro Ser Pro Leu Lys Lys
65 70 75 80

Val Asp Leu Pro Val Met Asn Ser Leu Thr His Gly Pro Met Phe Ser
85 90 95

Ser Ala Phe Ser Lys Pro Asp Leu Asn Phe Lys Gln Pro Thr Ile Ser
100 105 110

Leu Gln Gly Ile Pro Pro Asp Leu Phe Asp Arg Thr Ser Asp Phe Met
115 120 125

Val Ile Met Gly Ala Asn Gly Val Val Ile Thr Ile Trp Tyr Thr Ser
130 135 140

Pro Gly Asn Trp Leu Trp Gly Tyr Ser Leu Tyr Glu Ser Gly Asn Leu
145 150 155 160

Gly Gly Tyr Arg Val Trp Arg Leu Ile Leu Leu Pro Asn Asn Glu Val
165 170 175

Met Ile Val Asn Phe Asn Thr Arg Thr Thr Cys Ile Asn Thr Tyr Lys
180 185 190

Asn Gly Val Ile His Ser Pro Cys Asn Lys Asp Asn Pro Phe Gln Lys
195 200 205

Phe Thr Phe Arg Pro Met Thr Asn Gly Ala Val Gln Ile Tyr Asn Lys
210 215 220

Ala Thr Asn Cys Val Leu Ala Asn Ala Cys
225 230

<210> 53
<211> 284
<212> PRT
<213> *Campylobacter fetus*

<400> 53

Met Val Phe Ala Pro Ala Ala Ser Trp Lys Thr Ile Leu Leu Gly
1 5 10 15

Val Lys Met Arg Asn Val Ile Met Ile Ile Phe Ile Ala Thr Leu Gly
20 25 30

Phe Ala Lys Pro Glu Asp Tyr Lys Ile Ala Thr Trp Asn Leu Gln Gly
35 40 45

Ser Ser Ala Ile Thr Glu Ser Lys Trp Asn Ile Ser Val Arg Gln Ile
50 55 60

Ile Ser Gly Glu Asn Pro Ala Asp Ile Leu Ala Val Gln Glu Ala Gly
65 70 75 80

Asn Leu Pro Gln Thr Ala Leu Pro Thr Gly Arg Ser Ile Asn Gln Gly
85 90 95

Gly Thr Ile Val Thr Glu His Leu Trp Gln Leu Gly Ser Ile Ser Arg
100 105 110

Pro Phe Gln Val Tyr Ile Tyr Tyr Ala Gln Ile Asp Thr Gly Ala Asn
115 120 125

Arg Val Asn Leu Ala Ile Val Ser Arg Ile Lys Ala Asp Glu Ile Ile
130 135 140

Ile Leu Pro Pro Pro Thr Val Ala Ser Arg Pro Leu Ile Gly Ile Arg
145 150 155 160

Ile Gly Asn Asp Val Phe Phe Asn Ile His Ala Leu Ala Asn Gly Gly
165 170 175

Val Asp Ala Pro Ala Ile Ile Asn Ser Ile Phe Asp Arg Phe Arg Asn
180 185 190

Met Pro Asn Ile Thr Trp Met Ile Leu Gly Asp Phe Asn Arg Ser Pro
195 200 205

Glu Ser Leu Arg Gly Thr Leu Gly Leu Glu Thr Arg Val Arg Val Thr
210 215 220

Phe Leu Thr Pro Pro Ala Pro Thr Gln Arg Ser Gly Gly Thr Leu Asp
225 230 235 240

Trp Ala Ile Val Gly Asn Ser Ala Gly Asp Leu Val Arg Thr Thr Leu
245 250 255

Val Ala Val Leu Met Leu Ala Asn Leu Arg Thr His Leu Val Ser Asp
260 265 270

His Phe Pro Val Asn Phe Arg Lys Phe Gly Asp Asn
275 280

<210> 54
<211> 182
<212> PRT
<213> *Campylobacter fetus*

<400> 54

Met Lys Ala Leu Ala Ile Ile Phe Leu Phe Val Ser Ile Ser Phe Ala
1 5 10 15

Asn Glu Asn Ile Thr Asp Ala Phe Gln Ile Arg Asn Ala Asn Thr Gly
20 25 30

Ile Pro Ile Asn Ile Lys Arg Phe Ser Gly Gln Phe Asn Tyr Gln Asn
35 40 45

Trp Phe Leu Asn Asp Leu Gly Val Asp Pro Lys Ile Lys Lys Val Asp
50 55 60

Lys Phe Ser Asn Ser Phe Pro Phe Gly Tyr Val Gln Phe Gln Val Ala
65 70 75 80

Ala Asp Val Lys Met Cys Leu Gln Ile Ala Pro Ser Gly Phe Leu Ala
85 90 95

Leu Lys Asn Cys Lys Gln Asp Tyr Asp Ser Gly Glu Phe Glu Thr Ile
100 105 110

Phe Gln Ile Ile Pro Thr Ser Ser Gly Ala Met Gln Leu Arg Ser Leu
115 120 125

Val Leu Lys Thr Asn Glu Cys Leu Gly Thr Phe Glu Asn Pro Asn Val
130 135 140

Pro Ile Glu Asp Arg Val Gly Leu Val Arg Cys Val Leu Glu Phe Phe
145 150 155 160

Val Asp Ile Glu Pro Lys Gln Leu Phe Val Phe Ser Pro Pro Leu Ser
165 170 175

Glu Ala Lys Val Ile Arg
180

<210> 55
<211> 29
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<220>
<221> misc_feature
<222> (21)..(29)
<223> "n" indicates a, t, g, or ,c

<400> 55
gctttagca gtattgatgc nnnnnnnnn

29

<210> 56
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 56
gctttagca gtattgatgc

20

<210> 57
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 57
ctagttcg accatttcc

20

<210> 58
<211> 29
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<220>
<221> misc_feature
<222> (21)..(29)
<223> "n" indicates a, t, g, or ,c

<400> 58
atacgcaatg caaacaccgg nnnnnnnnnn 29

<210> 59
<211> 19
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 59
atacgcaatg aaacaccgg 19

<210> 60
<211> 21
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 60
taaaaagcgat tttcagggca g 21

<210> 61
<211> 29
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<220>
<221> misc_feature
<222> (21)..(29)
<223> "n" indicates a, t, g, or ,c

<400> 61
tgtcgacata gagcctaaac nnnnnnnnnn 29

<210> 62
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 62
tgtcgacata gaggctaaac 20

<210> 63
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 63
attttcacccg ccgccttagtg 20

<210> 64
<211> 34
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 64
gaaactgata cactaggata cgatccattc caaa 34

<210> 65
<211> 28
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 65
gaataatcag gtcgctttgc taatgaca 28

<210> 66
<211> 33
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 66
agcatgtctc atagatatgt actcaaaaact tgg 33

<210> 67
<211> 32
<212> DNA
<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 67

agcctaagta tccataaacgt cgtattcttt gc

32

<210> 68

<211> 20

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 68

aggacttgaa cctacttttc

20

<210> 69

<211> 20

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 69

aggtggagta gttaaaaacc

20

<210> 70

<211> 20

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 70

attgccaagg ctaaaatctc

20

<210> 71

<211> 18

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 71

gataaaagtct aaaactgc

18

<210> 72

<211> 20

<212> DNA

<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 72
aacgacaaat gtaaggactc 20

<210> 73
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 73
tatttatgca agtcgtgcga 20

<210> 74
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 74
tttagcctt gcaactccta 20

<210> 75
<211> 19
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 75
aagggttagc agctgttaa 19

<210> 76
<211> 21
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 76
tagggatat gcacgcaaaa g 21

<210> 77
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 77
gcttaataca gttacgatacg 20

<210> 78
<211> 20
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 78
aagcataagt tttgcaaacg 20

<210> 79
<211> 21
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 79
gtttggattt tcaaatgttc c 21